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RAW SEQUENCE LISTING

DATE: 07/23/2002

PATENT APPLICATION: US/10/025,145A

TIME: 15:54:32

Input Set : A:\WSUR18414Seq2.txt

Output Set: N:\CRF3\07232002\J025145A.raw

3 <110> APPLICANT: Croteau, Rodney B.
 4 Bohlmann, Joerg
 5 Steele, Christopher L.
 6 Phillips, Michael A.
 8 <120> TITLE OF INVENTION: Monoterpene Synthases from Grand Fir (Abies Grandis)
 10 <130> FILE REFERENCE: WSUR118414
 12 <140> CURRENT APPLICATION NUMBER: 10/025,145A
 C--> 13 <141> CURRENT FILING DATE: 2002-06-28
 15 <150> PRIOR APPLICATION NUMBER: US 09/360,545
 16 <151> PRIOR FILING DATE: 1999-07-26
 18 <150> PRIOR APPLICATION NUMBER: PCT/US98/14528
 19 <151> PRIOR FILING DATE: 1998-07-10
 21 <150> PRIOR APPLICATION NUMBER: US 60/052,249
 22 <151> PRIOR FILING DATE: 1997-07-11
 24 <160> NUMBER OF SEQ ID NOS: 107
 26 <170> SOFTWARE: PatentIn version 3.1
 28 <210> SEQ ID NO: 1
 29 <211> LENGTH: 2196
 30 <212> TYPE: DNA
 31 <213> ORGANISM: Abies Grandis
 33 <220> FEATURE:
 34 <221> NAME/KEY: CDS
 35 <222> LOCATION: (69)..(1952)
 36 <223> OTHER INFORMATION:
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 43 Met Ala Leu Val Ser Ile Ser Pro Leu Ala Ser Lys Ser Cys
 44 1 5 10
 46 ctg cgc aag tcg ttg atc agt tca att cat gaa cat aag cct ccc tat 158
 47 Leu Arg Lys Ser Leu Ile Ser Ser Ile His Glu His Lys Pro Pro Tyr
 48 15 20 25 30
 50 aga aca atc cca aat ctt gga atg cgt agg cga ggg aaa tct gtc acg 206
 51 Arg Thr Ile Pro Asn Leu Gly Met Arg Arg Arg Gly Lys Ser Val Thr
 52 35 40 45
 54 cct tcc atg agc atc agt ttg gcc acc gct gca cct gat gat ggt gta 254
 55 Pro Ser Met Ser Ile Ser Leu Ala Thr Ala Ala Pro Asp Asp Gly Val
 56 50 55 60
 58 caa aga cgc ata ggt gac tac cat tcc aat atc tgg gac gat gat ttc 302
 59 Gln Arg Arg Ile Gly Asp Tyr His Ser Asn Ile Trp Asp Asp Asp Phe
 60 65 70 75
 62 ata cag tct cta tca acg cct tat ggg gaa ccc tct tac cag gaa cgt 350
 63 Ile Gln Ser Leu Ser Thr Pro Tyr Gly Glu Pro Ser Tyr Gln Glu Arg

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64	80	85	90	
66	gct gag aga tta att gtg gag gta aag aag ata ttc aat tca atg tac	398		
67	Ala Glu Arg Leu Ile Val Glu Val Lys Lys Ile Phe Asn Ser Met Tyr			
68	95	100	105	110
70	ctg gat gat gga aga tta atg agt tcc ttt aat gat ctc atg caa cgc	446		
71	Leu Asp Asp Gly Arg Leu Met Ser Ser Phe Asn Asp Leu Met Gln Arg			
72		115	120	125
74	ctt tgg ata gtc gat agc gtt gaa cgt ttg ggg ata gct aga cat ttc	494		
75	Leu Trp Ile Val Asp Ser Val Glu Arg Leu Gly Ile Ala Arg His Phe			
76		130	135	140
78	aag aac gag ata aca tca gct ctg gat tat gtt ttc cgt tac tgg gag	542		
79	Lys Asn Glu Ile Thr Ser Ala Leu Asp Tyr Val Phe Arg Tyr Trp Glu			
80		145	150	155
82	gaa aac ggc att gga tgt ggg aga gac agt att gtt act gat ctc aac	590		
83	Glu Asn Gly Ile Gly Cys Gly Arg Asp Ser Ile Val Thr Asp Leu Asn			
84		160	165	170
86	tca act gcg ttg ggg ttt cga act ctt cga tta cac ggg tac act gta	638		
87	Ser Thr Ala Leu Gly Phe Arg Thr Leu Arg Leu His Gly Tyr Thr Val			
88	175	180	185	190
90	tct cca gag gtt tta aaa gct ttt caa gat caa aat gga cag ttt gta	686		
91	Ser Pro Glu Val Leu Lys Ala Phe Gln Asp Gln Asn Gly Gln Phe Val			
92		195	200	205
94	tgc tcc ccc ggt cag aca gag ggt gag atc aga agc gtt ctt aac tta	734		
95	Cys Ser Pro Gly Gln Thr Glu Gly Glu Ile Arg Ser Val Leu Asn Leu			
96		210	215	220
98	tat cgg gct tcc ctc att gcc ttc cct ggt gag aaa gtt atg gaa gaa	782		
99	Tyr Arg Ala Ser Leu Ile Ala Phe Pro Gly Glu Lys Val Met Glu Glu			
100		225	230	235
102	gct gaa atc ttc tcc aca aga tat ttg aaa gaa gct cta caa aag att	830		
103	Ala Glu Ile Phe Ser Thr Arg Tyr Leu Lys Glu Ala Leu Gln Lys Ile			
104		240	245	250
106	cca gtc tcc gct ctt tca caa gag ata aag ttt gtt atg gaa tat ggc	878		
107	Pro Val Ser Ala Leu Ser Gln Glu Ile Lys Phe Val Met Glu Tyr Gly			
108	255	260	265	270
110	tgg cac aca aat ttg cca aga ttg gaa gca aga aat tac ata gac aca	926		
111	Trp His Thr Asn Leu Pro Arg Leu Glu Ala Arg Asn Tyr Ile Asp Thr			
112		275	280	285
114	ctt gag aaa gac acc agt gca tgg ctc aat aaa aat gct ggg aag aag	974		
115	Leu Glu Lys Asp Thr Ser Ala Trp Leu Asn Lys Asn Ala Gly Lys Lys			
116		290	295	300
118	ctt tta gaa ctt gca aaa ttg gag ttc aat ata ttt aac tcc tta caa	1022		
119	Leu Leu Glu Leu Ala Lys Leu Glu Phe Asn Ile Phe Asn Ser Leu Gln			
120		305	310	315
122	caa aag gaa tta caa tat ctt ttg aga tgg tgg aaa gag tcg gat ttg	1070		
123	Gln Lys Glu Leu Gln Tyr Leu Leu Arg Trp Trp Lys Glu Ser Asp Leu			
124		320	325	330
126	cct aaa ttg aca ttt gct cgg cat cgt cat gtg gaa ttc tac act ttg	1118		
127	Pro Lys Leu Thr Phe Ala Arg His Arg His Val Glu Phe Tyr Thr Leu			
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130	gcc	tct	tgt	att	gcc	att	gac	cca	aaa	cat	tct	gca	ttc	aga	cta	ggc	1166
131	Ala	Ser	Cys	Ile	Ala	Ile	Asp	Pro	Lys	His	Ser	Ala	Phe	Arg	Leu	Gly	
132					355					360						365	
134	ttc	gcc	aaa	atg	tgt	cat	ctt	gtc	aca	ggt	ttg	gac	gat	att	tac	gac	1214
135	Phe	Ala	Lys	Met	Cys	His	Leu	Val	Thr	Val	Leu	Asp	Asp	Ile	Tyr	Asp	
136				370					375					380			
138	act	ttt	gga	acg	att	gac	gag	ctt	gaa	ctc	ttc	aca	tct	gca	att	aag	1262
139	Thr	Phe	Gly	Thr	Ile	Asp	Glu	Leu	Glu	Leu	Phe	Thr	Ser	Ala	Ile	Lys	
140			385					390					395				
142	aga	tgg	aat	tca	tca	gag	ata	gaa	cac	ctt	cca	gaa	tat	atg	aaa	tgt	1310
143	Arg	Trp	Asn	Ser	Ser	Glu	Ile	Glu	His	Leu	Pro	Glu	Tyr	Met	Lys	Cys	
144		400					405					410					
146	gtg	tac	atg	gtc	gtg	ttt	gaa	act	gta	aat	gaa	ctg	aca	cga	gag	gcg	1358
147	Val	Tyr	Met	Val	Val	Phe	Glu	Thr	Val	Asn	Glu	Leu	Thr	Arg	Glu	Ala	
148	415					420					425				430		
150	gag	aag	act	caa	ggg	aga	aac	act	ctc	aac	tat	gtt	cga	aag	gct	tgg	1406
151	Glu	Lys	Thr	Gln	Gly	Arg	Asn	Thr	Leu	Asn	Tyr	Val	Arg	Lys	Ala	Trp	
152				435					440					445			
154	gag	gct	tat	ttt	gat	tca	tat	atg	gaa	gaa	gca	aaa	tgg	atc	tct	aat	1454
155	Glu	Ala	Tyr	Phe	Asp	Ser	Tyr	Met	Glu	Glu	Ala	Lys	Trp	Ile	Ser	Asn	
156			450						455				460				
158	ggg	tat	ctg	cca	atg	ttt	gaa	gag	tac	cat	gag	aat	ggg	aaa	gtg	agc	1502
159	Gly	Tyr	Leu	Pro	Met	Phe	Glu	Glu	Tyr	His	Glu	Asn	Gly	Lys	Val	Ser	
160		465					470					475					
162	tct	gca	tat	cgc	gta	gca	aca	ttg	caa	ccc	atc	ctc	act	ttg	aat	gca	1550
163	Ser	Ala	Tyr	Arg	Val	Ala	Thr	Leu	Gln	Pro	Ile	Leu	Thr	Leu	Asn	Ala	
164		480				485					490						
166	tgg	ctt	cct	gat	tac	atc	ttg	aag	gga	att	gat	ttt	cca	tcc	agg	ttc	1598
167	Trp	Leu	Pro	Asp	Tyr	Ile	Leu	Lys	Gly	Ile	Asp	Phe	Pro	Ser	Arg	Phe	
168	495					500					505				510		
170	aat	gat	ttg	gca	tcg	tcc	ttc	ctt	cgg	cta	cga	ggt	gac	aca	cgc	tgc	1646
171	Asn	Asp	Leu	Ala	Ser	Ser	Phe	Leu	Arg	Leu	Arg	Gly	Asp	Thr	Arg	Cys	
172				515					520				525				
174	tac	aag	gcc	gat	agg	gat	cgt	ggt	gaa	gaa	gct	tcg	tgt	ata	tca	tgt	1694
175	Tyr	Lys	Ala	Asp	Arg	Asp	Arg	Gly	Glu	Glu	Ala	Ser	Cys	Ile	Ser	Cys	
176			530						535				540				
178	tat	atg	aaa	gac	aat	cct	gga	tca	acc	gaa	gaa	gat	gcc	ctc	aat	cat	1742
179	Tyr	Met	Lys	Asp	Asn	Pro	Gly	Ser	Thr	Glu	Glu	Asp	Ala	Leu	Asn	His	
180			545					550					555				
182	atc	aat	gcc	atg	gtc	aat	gac	ata	atc	aaa	gaa	tta	aat	tgg	gaa	ctt	1790
183	Ile	Asn	Ala	Met	Val	Asn	Asp	Ile	Ile	Lys	Glu	Leu	Asn	Trp	Glu	Leu	
184		560					565					570					
186	cta	aga	tcc	aac	gac	aat	att	cca	atg	ctg	gcc	aag	aaa	cat	gct	ttt	1838
187	Leu	Arg	Ser	Asn	Asp	Asn	Ile	Pro	Met	Leu	Ala	Lys	Lys	His	Ala	Phe	
188	575					580					585				590		
190	gac	ata	aca	aga	gct	ctc	cac	cat	ctc	tac	ata	tat	cga	gat	ggc	ttt	1886
191	Asp	Ile	Thr	Arg	Ala	Leu	His	His	Leu	Tyr	Ile	Tyr	Arg	Asp	Gly	Phe	
192				595					600						605		
194	agt	ggt	gcc	aac	aag	gaa	aca	aaa	aaa	ttg	ggt	atg	gaa	aca	ctc	ctt	1934

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195 Ser Val Ala Asn Lys Glu Thr Lys Lys Leu Val Met Glu Thr Leu Leu
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199 Glu Ser Met Leu Phe
200                               625
202 aatgctaaat tattggcctt atgacatagt ttatgtatgt acttgtgtga attcaatcat      2042
204 atcgtgtggg tatgattaaa aagctagagc ttactagggt agtaacatgg tgataaaagt      2102
206 tataaaatgt gagttataga gatacccatg ttgaataatg aattacaaaa agagaaattt      2162
208 atgtagaata agattggaag cttttcaatt gttt      2196
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212 <211> LENGTH: 627
213 <212> TYPE: PRT
214 <213> ORGANISM: Abies Grandis
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223                               20                25                30
226 Ile Pro Asn Leu Gly Met Arg Arg Arg Gly Lys Ser Val Thr Pro Ser
227                               35                40                45
230 Met Ser Ile Ser Leu Ala Thr Ala Ala Pro Asp Asp Gly Val Gln Arg
231                               50                55                60
234 Arg Ile Gly Asp Tyr His Ser Asn Ile Trp Asp Asp Asp Phe Ile Gln
235 65                               70                75                80
238 Ser Leu Ser Thr Pro Tyr Gly Glu Pro Ser Tyr Gln Glu Arg Ala Glu
239                               85                90                95
242 Arg Leu Ile Val Glu Val Lys Lys Ile Phe Asn Ser Met Tyr Leu Asp
243                               100               105               110
246 Asp Gly Arg Leu Met Ser Ser Phe Asn Asp Leu Met Gln Arg Leu Trp
247                               115               120               125
250 Ile Val Asp Ser Val Glu Arg Leu Gly Ile Ala Arg His Phe Lys Asn
251                               130               135               140
254 Glu Ile Thr Ser Ala Leu Asp Tyr Val Phe Arg Tyr Trp Glu Glu Asn
255 145                               150               155               160
258 Gly Ile Gly Cys Gly Arg Asp Ser Ile Val Thr Asp Leu Asn Ser Thr
259                               165               170               175
262 Ala Leu Gly Phe Arg Thr Leu Arg Leu His Gly Tyr Thr Val Ser Pro
263                               180               185               190
266 Glu Val Leu Lys Ala Phe Gln Asp Gln Asn Gly Gln Phe Val Cys Ser
267                               195               200               205
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271                               210               215               220
274 Ala Ser Leu Ile Ala Phe Pro Gly Glu Lys Val Met Glu Glu Ala Glu
275 225                               230               235               240
278 Ile Phe Ser Thr Arg Tyr Leu Lys Glu Ala Leu Gln Lys Ile Pro Val
279                               245               250               255
282 Ser Ala Leu Ser Gln Glu Ile Lys Phe Val Met Glu Tyr Gly Trp His
283                               260               265               270
286 Thr Asn Leu Pro Arg Leu Glu Ala Arg Asn Tyr Ile Asp Thr Leu Glu

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287          275          280          285
290 Lys Asp Thr Ser Ala Trp Leu Asn Lys Asn Ala Gly Lys Lys Leu Leu
291          290          295          300
294 Glu Leu Ala Lys Leu Glu Phe Asn Ile Phe Asn Ser Leu Gln Gln Lys
295 305          310          315          320
298 Glu Leu Gln Tyr Leu Leu Arg Trp Trp Lys Glu Ser Asp Leu Pro Lys
299          325          330          335
302 Leu Thr Phe Ala Arg His Arg His Val Glu Phe Tyr Thr Leu Ala Ser
303          340          345          350
306 Cys Ile Ala Ile Asp Pro Lys His Ser Ala Phe Arg Leu Gly Phe Ala
307          355          360          365
310 Lys Met Cys His Leu Val Thr Val Leu Asp Asp Ile Tyr Asp Thr Phe
311          370          375          380
314 Gly Thr Ile Asp Glu Leu Glu Leu Phe Thr Ser Ala Ile Lys Arg Trp
315 385          390          395          400
318 Asn Ser Ser Glu Ile Glu His Leu Pro Glu Tyr Met Lys Cys Val Tyr
319          405          410          415
322 Met Val Val Phe Glu Thr Val Asn Glu Leu Thr Arg Glu Ala Glu Lys
323          420          425          430
326 Thr Gln Gly Arg Asn Thr Leu Asn Tyr Val Arg Lys Ala Trp Glu Ala
327          435          440          445
330 Tyr Phe Asp Ser Tyr Met Glu Glu Ala Lys Trp Ile Ser Asn Gly Tyr
331          450          455          460
334 Leu Pro Met Phe Glu Glu Tyr His Glu Asn Gly Lys Val Ser Ser Ala
335 465          470          475          480
338 Tyr Arg Val Ala Thr Leu Gln Pro Ile Leu Thr Leu Asn Ala Trp Leu
339          485          490          495
342 Pro Asp Tyr Ile Leu Lys Gly Ile Asp Phe Pro Ser Arg Phe Asn Asp
343          500          505          510
346 Leu Ala Ser Ser Phe Leu Arg Leu Arg Gly Asp Thr Arg Cys Tyr Lys
347          515          520          525
350 Ala Asp Arg Asp Arg Gly Glu Glu Ala Ser Cys Ile Ser Cys Tyr Met
351          530          535          540
354 Lys Asp Asn Pro Gly Ser Thr Glu Glu Asp Ala Leu Asn His Ile Asn
355 545          550          555          560
358 Ala Met Val Asn Asp Ile Ile Lys Glu Leu Asn Trp Glu Leu Leu Arg
359          565          570          575
362 Ser Asn Asp Asn Ile Pro Met Leu Ala Lys Lys His Ala Phe Asp Ile
363          580          585          590
366 Thr Arg Ala Leu His His Leu Tyr Ile Tyr Arg Asp Gly Phe Ser Val
367          595          600          605
370 Ala Asn Lys Glu Thr Lys Lys Leu Val Met Glu Thr Leu Leu Glu Ser
371          610          615          620
374 Met Leu Phe
375 625
378 <210> SEQ ID NO: 3
379 <211> LENGTH: 2018
380 <212> TYPE: DNA
381 <213> ORGANISM: Abies Grandis

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/025,145A

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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Seq#:8; N Pos. 6,12
Seq#:9; N Pos. 3,6,9,12
Seq#:10; N Pos. 7,8,9,18
Seq#:13; N Pos. 89
Seq#:14; N Pos. 93
Seq#:21; N Pos. 3,12
Seq#:22; N Pos. 6,12,15,18
Seq#:23; N Pos. 7,10,16
Seq#:25; Xaa Pos. 3,4,6,8
Seq#:26; Xaa Pos. 3,4,6
Seq#:27; Xaa Pos. 2,3,4
Seq#:28; Xaa Pos. 6
Seq#:45; Xaa Pos. 3,4
Seq#:46; Xaa Pos. 4
Seq#:50; Xaa Pos. 1
Seq#:51; Xaa Pos. 1
Seq#:52; Xaa Pos. 1
Seq#:53; Xaa Pos. 6
Seq#:56; N Pos. 1,4,7